AMENDMENTS TO THE SPECIFICATION:

Please replace paragraph [13] with the following replacement paragraph:

[13] In yet another embodiment of the invention, a method is provided to produce a plant tolerant to stress conditions comprising the steps of providing plant cells with a chimeric gene to create transgenic plant cells, comprising a DNA region, which when transcribed yields an ParG inhibitory RNA molecule, whereby the DNA region comprises a nucleotide sequence of at least 21 to 100 nucleotides of a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID No. 1, 2 or 16 or at least 21 to 100 nucleotides of a nucleotide sequence of SEQ ID No. 3, 4, 15 or 23 operably linked to a plant-expressible promoter and a 3' end region involved in transcription termination and polyadenylation; regenerating a population of transgenic plant lines from said transgenic plant cell; and identifying a stress tolerant plant line within the population of transgenic plant lines.

Please replace paragraph [14] with the following replacement paragraph:

[14] The invention also provides DNA molecules comprising a plant-expressible promoter, operably linked to a DNA region, which when transcribed yields an ParG inhibitory RNA molecule, and to a 3' end region involved in transcription termination and polyadenylation. The ParG inhibitory RNA molecule may comprise a nucleotide sequence of at least 20 consecutive nucleotides of the nucleotide sequence of the ParG gene present in the plant cell (the endogenous ParG gene). The ParG inhibitory RNA molecule may also comprise a nucleotide sequence of at least 20 consecutive nucleotides of the complement of the nucleotide sequence of the ParG gene present in the plant cell (the endogenous ParG gene). In yet another embodiment, the parG inhibitory RNA may comprise a sense region comprising a nucleotide sequence of at least 20 consecutive nucleotides of the nucleotide sequence of the ParG gene present in the plant cell and an antisense region comprising a nucleotide sequence of at least 20 consecutive nucleotides of the complement of the nucleotide sequence of the ParG gene present in the plant cell, wherein the sense and antisense region are capable of forming a double stranded RNA region comprising said at least 20 consecutive nucleotides. The chimeric gene may further comprise a DNA region encoding a self-splicing ribozyme between said DNA region coding for parG inhibitory RNA molecule and the 3' end region. The chimeric gene may also comprise a nucleotide sequence of at least 21 to 100 nucleotides of a nucleotide sequence encoding a protein comprising the amino

acid sequence of SEQ ID No 1, 2 or 16 or at least 21 to 100 nucleotides of a nucleotide sequence of SEQ ID No. 3, 4, 15 or 23.

Please replace paragraph [29] with the following replacement paragraph:

[29] PARG encoding genes may comprise a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID No. 1 (Arabidopsis thaliana) or of SEQ ID No. 2 (Solanum tuberosum) or of SEQ ID No. 16 (Oryza sativa) or parts thereof, such as a DNA fragment comprising the nucleotide sequence of SEQ ID No. 3 or SEQ ID No. 4 or SEQ ID No. 15. or SEQ ID No. 23 (Zea mays).

Please replace paragraph [35] with the following replacement paragraph:

[35] However, it will be clear that the skilled person can isolate variant DNA sequences from other plant species, by hybridization with a probe derived from the above mentioned PARG encoding genes from plant species, or even with a probe derived from the above mentioned PARG encoding genes from animal species. To this end, the probes should preferably have a nucleotide sequence comprising at least 40 consecutive nucleotides from the coding region of those mentioned PARG encoding genes sequences, preferably from the coding region of SEQ ID No 3 or SEQ ID No 4. The probes may however comprise longer regions of nucleotide sequences derived from the ParG genes, such as about 50, 60, 75, 100, 200 or 500 consecutive nucleotides from any of the mentioned ParG genes. Preferably, the probe should comprise a nucleotide sequence coding for one of the highly conserved regions of the catalytic domain, which have been identified by aligning the different PARG proteins from animals. These regions are also present in the identified PARG protein from Arabidopsis thaliana and comprise the amino acid sequence LXVDFANXXXGGG (SEQ ID No. 10 from the amino acid at position 1 to the amino acid at position 13; corresponding to SEQ ID No 1 from the amino acid at position 252 to the amino acid at position 264; X may be any amino acid) LXVDFANXXXGGGXXXXGXVQEEIRF (SEQ ID No. 10 from the amino acid at position 1 to the amino acid at position 26; corresponding to SEQ ID No 1 from the amino acid at position 252 to the amino acid at position 277) or LXVDFANXXXGGGXXXXGXVQEEIRFXXXPE (SEQ ID No. 10; corresponding to SEQ ID No 1 from the amino acid at position 252 to the amino acid at position 282), TGXWGCGXFXGD (SEQ ID No. 11 from the amino acid at

position 1 to the amino acid at position 12; corresponding to SEQ ID No 1 from the amino acid at position 449 to the amino acid at position 460) or TGXWGCGAFXGDXXLKXXXQ (SEQ ID No. 11; corresponding to SEQ ID No 1 from the amino acid at position 449 to the amino acid at position 468). Other conserved regions have the amino acid sequence DXXXRXXXXAIDA (SEQ ID No. 12; corresponding to SEQ ID No 1 from the amino acid at position 335 to the amino acid at position 344) or REXXKAXXGF (SEQ ID No. 13; corresponding to SEQ ID No 1 from the amino acid at position 360 to the amino acid at position 369) or GXXXXSXYTGY (SEQ ID No. 14; corresponding to SEQ ID No 1 from the amino acid at position 303 to the amino acid at position 313). Hybridization should preferably be under stringent conditions.